



SEQUENCE LISTING

<110> Guerry, Patricia
Trust, Trevor J
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Lee, Lanfong

<120> A Recombinant Polypeptide for use in the Manufacture of Vaccines
against Campylobacter Induced Diarrhea and to Reduce Colonization

<130> 78560

<140> 09/439,311

<141> 1999-11-12

<150> US 60/108,114

<151> 1998-11-12

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<210> 1

<211> 999

<212> DNA

<213> Campylobacter coli

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JAN 08 2002

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<213> *Campylobacter coli*

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 35 40 45
 Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr Leu Gly Gln Ala
 50 55 60
 Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu Gln Thr Ala Asp
 65 70 75
 Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Ile Lys Thr
 80 85 90
 Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser Leu Lys Thr Arg
 95 100 105
 Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met Glu Glu Leu Asp
 110 115 120
 Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys Gln Leu Leu Ser
 125 130 135
 Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly Ser Ser Ser Asn
 140 145 150
 Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln Ser Ser Lys Ile
 155 160 165
 Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser Phe Ser Ser Gly
 170 175 180
 Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly Ile Glu Asp Phe
 185 190 195
 Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val Gly Thr Gly Leu
 200 205 210
 Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala Asp Lys Thr Gly
 215 220 225
 Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly Ala Tyr Ala Ile
 230 235 240
 Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile Asn Gly Val Val
 245 250 255

Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu Asn Gly Ser Leu
 260 265 270
 Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr Gly Val Gln Ala
 275 280 285
 Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr Ser Ala Asp Gly
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 Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val Gly Ala Gly Ile
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<213> *Campylobacter coli*

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<213> *Campylobacter jejuni* 81-176

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 35 40 45
 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr
 50 55 60
 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu
 65 70 75
 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp
 80 85 90
 Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser
 95 100 105
 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met
 110 115 120
 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys
 125 130 135
 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly
 140 145 150
 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln
 155 160 165
 Ser Ser Lys Ile Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser
 170 175 180
 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly
 185 190 195
 Ile Glu Asp Phe Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val
 200 205 210
 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala
 215 220 225
 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly
 230 235 240
 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile
 245 250 255
 Asn Gly Val Val Ile Gly Gln Ile Asn Tyr Asn Asp Gly Asp Asn
 260 265 270
 Asn Gly Gln Leu Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr
 275 280 285
 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr
 290 295 300
 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val
 305 310 315
 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu
 320 325 330
 Val Lys Asn Asp Gly Arg Asp Ile Asn Ile Ser Gly Thr Gly Leu
 335 340 345
 Ser Ala Ile Gly Met Gly Ala Thr Asp Met Ile Ser Gln Ser Ser
 350 355 360
 Val Ser Leu Arg Glu Ser Lys Gly Gln Ile Ser Ala Ala Asn Ala
 365 370 375

Asp Ala Met Gly Phe Asn Ser Tyr Lys Gly Gly Gly Lys Phe Val
 380 385 390
 Phe Thr Gln Asn Val Ser Ser Ile Ser Ala Phe Met Ser Ala Gln
 395 400 405
 Gly Ser Gly Phe Ser Arg Gly Ser Gly Phe Ser Val Gly Ser Gly
 410 415 420
 Lys Asn Leu Ser Val Gly Leu Ser Gln Gly Ile Gln Ile Ile Ser
 425 430 435
 Ser Ala Ala Ser Met Ser Asn Thr Tyr Val Val Ser Ala Gly Ser
 440 445 450
 Gly Phe Ser Ser Gly Ser Gly Asn Ser Gln Phe Ala Ala Leu Lys
 455 460 465
 Thr Thr Ala Ala Asn Thr Thr Asp Glu Thr Ala gly Val Thr Thr
 470 475 480
 Leu Lys Gly Ala Met Ala Val Met Asp Ile Ala Glu Thr Ala Ile
 485 490 495
 Thr Asn Leu Asp Gln Ile Arg Ala Asp Ile Gly Ser Ile Gln Asn
 500 505 510
 Gln Val Thr Ser Thr Ile Asn Asn Ile Thr Val Thr Gln Val Asn
 515 520 525
 Val Lys Ala Ala Glu Ser Gln Ile Arg Asp Val Asp Phe Ala Ser
 530 535 540
 Glu Ser Ala Asn Tyr Ser Lys Ala Asn Ile Leu Ala Gln Ser Gly
 545 550 555
 Ser Tyr Ala Met Ala Gln Ala Asn Ser Ser Gln Gln Asn Val Leu
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 Arg Leu Leu Gln

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<211> 573

<212> PRT

<213> *Campylobacter coli* VC167 T2

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 Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala
 35 40 45
 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr
 50 55 60
 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu
 65 70 75
 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp
 80 85 90

Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser
 95 100 105
 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met
 110 115 120
 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys
 125 130 135
 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly
 140 145 150
 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln
 155 160 165
 Ser Ser Lys Ile Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser
 170 175 180
 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly
 185 190 195
 Ile Glu Asp Phe Lys Phe Gln Ser Val Val Ile Ser Thr Ser Val
 200 205 210
 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala
 215 220 225
 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly
 230 235 240
 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile
 245 250 255
 Asn Gly Val Val Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu
 260 265 270
 Asn Gly Ser Leu Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr
 275 280 285
 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr
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 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val
 305 310 315
 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu
 320 325 330
 Val Lys Asn Asp Gly Arg Asp Ile Asn Ile Ser Gly Thr Gly Leu
 335 340 345
 Ser Ala Ile Gly Met Gly Ala Thr Asp Met Ile Ser Gln Ser Ser
 350 355 360
 Val Ser Leu Arg Glu Ser Lys Gly Gln Ile Ser Ala Ala Asn Ala
 365 370 375
 Asp Ala Met Gly Phe Asn Ala Tyr Asn Gly Gly Ala Lys Gln
 380 385 390
 Ile Ile Phe Ala Ser Ser Ile Ala Gly Phe Met Ser Gln Ala Gly
 395 400 405
 Ser Gly Phe Ser Ala Gly Ser Gly Phe Ser Val Gly Ser Gly Lys
 410 415 420
 Asn Tyr Ser Ala Ile Leu Ser Ala Ser Ile Gln Ile Val Ser Ser
 425 430 435
 Ala Arg Ser Ile Ser Ser Thr Tyr Val Val Ser Thr Gly Ser Gly
 440 445 450
 Phe Ser Ala Gly Ser Gly Asn Ser Gln Phe Ala Ala Leu Arg Ile
 455 460 465
 Ser Thr Val Ser Ala His Asp Glu Thr Ala Gly Val Thr Thr Leu
 470 475 480
 Lys Gly Ala Met Ala Val Met Asp Ile Ala Glu Thr Ala Ile Thr
 485 490 495

Asn Leu Asp Gln Ile Arg Ala Asp Ile Gly Ser Val Gln Asn Gln
500 505 510
Ile Thr Ser Thr Ile Asn Asn Ile Thr Val Thr Gln Val Asn Val
515 520 525
Lys Ser Ala Glu Ser Gln Ile Arg Asp Val Asp Phe Ala Ser Glu
530 535 540
Ser Ala Asn Tyr Ser Lys Ala Asn Ile Leu Ala Gln Ser Gly Ser
545 550 555
Tyr Ala Met Ala Gln Ala Asn Ser Ser Gln Gln Asn Val Leu Arg
560 565 570
Leu Leu Gln

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